Amendments to the Specification:

Please replace the paragraph beginning at page 4, line 1, with the following amended paragraph:

The structure of a hexapeptide (Boc-CL-Aib-AVC-NMe) [SEQ ID NO: 11] was determined crystallographically, revealing a type II' turn and β-sheet geometry. Karle *et al. J. Am. Chem. Soc.* (1988) **110**:1958-1963. An octapeptide with the same cysteine spacing was studied by NMR, and has a similar structure with a turn centered on Pro-Gly. Walse *et al.* (1996) *J. Comput.-Aided Mol. Des.* **10**:11-22. Peptides of the form Ac-CXPGXC-NMe [SEQ ID NO: 12] were evaluated by measurement of disulfide exchange equilibria, which indicated turn preferences between peptides of as much as 1 kcal/mol. Milburn *et al.* (1987) *J. Am. Chem. Soc.* **109**:4486-4496.

Please replace the paragraph beginning at page 4, line 14, with the following amended paragraph:

Disulfide-cyclized peptides from the hairpin region of a rabbit defensin have antibacterial activity exceeding (about 5 to 10-fold) that of the linear analogs. Circular dichroism spectroscopy indicates some non-random structure in phosphate buffer. The more potent peptide (CAGFMRIRGRIHPLCMRR) [SEQ ID NO: 13] has a Gly-Pro pair at the nonhydrogen-bonded sites nearest to the cysteines. Thennarasu & Nagaraj (1999) *Biochem. Biophys. Res. Commun.* **254**:281-283.

Please replace the paragraph beginning at page 26, line 2, with the following amended paragraph:

Spectra were acquired with an Aviv Instruments, Inc. Model 202 spectrophotometer. Peptide concentrations were determined spectrophotometrically as described in Gill & von Hippel (1989) *Anal. Biochem.* **182**:319-326. Melting curves were acquired at 229 nm with 1.5 min equilibration at each temperature and an averaging time of 15 s. Thermal denaturation was reversible, as judged by recovery of CD signal (≥95%) upon cooling. In addition, reverse melting curves were acquired for trpzips 1 and 4. Reverse and forward curves were identical in

shape, with $\leq$0.5 K shift in T_m. As a model for the unfolded state of the peptides, the melting curve (linear) of an equimolar mixture of the trpzip1 half peptides SWTWEG[SEQ ID NO: 14] and NKWTWK [SEQ ID NO: 15] was measured. Data for the trpzip peptides were then fit to a two-state unfolding equilibrium as described in Minor & Kim (1994) *Nature* **367**:660-663, fixing the unfolded baseline. Folded baselines, T_m, ΔH_m (ΔH at T_m), and ΔC_p were allowed to vary. For trpzips 5 and 6, the unfolded baseline could be fit directly to the experimental data. ΔS_m was calculated from the fit parameters (ΔH_m / T_m). Errors in Table 2 were generated by the fitting algorithm (Kaleidagraph, Synergy Software) and were given to indicate the quality of the fits to the particular experimental data set. However, when fitting different data sets, ΔH_m and ΔCp values varied by ~ 10%, as is typical in thermal denaturation experiments. Becktel & Schellman (1987) *Biopolymers* **26**:1859-1877.

Please replace the paragraph beginning at page 28, line 19, with the following amended paragraph:

The peptide trpzip1 (Table 1) consists of a representative type II′ turn sequence (EGNK) [SEQ ID NO: 16] flanked by the sequence WTW. An additional residue was added to each end of the peptide to permit cross-strand hydrogen bonding between the termini. Residues in hydrogen-bonded positions of the strands were taken from sequences used in our previous studies (WO 00/77194). Surprisingly, given that one-third of the residues are tryptophan, the peptide is freely soluble in water at millimolar concentrations. Trpzip1 has an unusual CD spectrum with intense exciton coupled bands at 215 and 229 nm (Fig. 1A), indicating interaction between the aromatic chromophores. Furthermore, the near UV CD spectrum of trpzip1 has well defined bands at the longer wavelength absorption maxima of tryptophan (Fig. 1A, inset), indicating that the indole side chains are in a defined chiral environment. In proteins, such near UV CD bands are often taken as evidence for fixed tertiary structure.